Evolutionary pattern of the genus *Salvia* L.

Fatemeh.Moein[a1]*, MohammadReza.Rahiminejad[a], Ziba.Jamzad[b], Douglas.Soltis[c], Pamela.Soltis[c]

a Department of Biology, Faculty of Science, University of Isfahan, Iran

b Department of Botany, Research institute of Forest and Rangelands, Tehran, Iran

c Department of Biology, University of Florida, Gainesville, FL, USA

* fatemeh.moein@gmail.com

Abstract: Bridging statistical model based method with molecular data provide new opportunity to answer one of the main question in biology whether higher richness and diversity in some organism's lineage is correlated to special traits effect. Angosperms as amajor group of seed plants have huge diversity and include high rate of diversification. Lamiaceae is the sixth largest family among Angiosperms with over 7000 speies distributed in all over the world. *Salvia* is known as the largest genus in this family including around 1000 species, having two stamens and speial pollination system reffered to as lever mechanism. This character evolved in parallel between the Old World and New World *Salvia* species. A high percentage of endemism and high morphological diversity are of special interest in understanding the evolutionary patterns within *Salvia*. Compared to New and Old World *Salvia*, taxa from Southwest Asia have not been well sampled in previous phylogenetic studies. In this study the phylogenetic relationships of Iranian species of *Salvi*a are reported for the first time. Iran contains 62 species of *Salvia* of which 19 are endemic and the area is considered as a center of diversity for *Salvia* in Southwest Asia. In current study, we used the supermatrix of 2 nuclear regions and three chloroplast regions for 250 taxa including 58 of Iranian species to reconstruct the phylogenetic tree in *Salvia* lineage. Maximum likelihood analysis was performed by RAxML v.8. Our analyses suggest that Iranian *Salvia* species are not monophyletic and instead they are placed in three main clades. To recounstruct the floral traits, we use the phytools package in phytools package of R, make.simmap function was used for reconstructing discrete charater and fitMk for continuous trait (Corlla length and Tube legth). Linage through time plot diversification have been done by applying ape, laser and DDD packages in R. we also test the effect of corolla length for the role of adaptive radiation in diversification of the genus *Salvia*, Although we did not achieve early burst of diversification, The rates of subclade diversification are higher than expected under Brownian mode. Since the main subclades have separate geographical ranges, overlap in morphospace is not equal to ecological overlap. We assume independent radiation of subclades among *Salvia* species. In addition, biogeographic patterns of *Salvia* in Old World will be discussed and effects of floral traits on diversification will be discussed.

Keywords: Salvia; diversification; phylogeny; Ancestral reconstruction

References

[1] Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and postanalysis of large phylogenies. Bioinformatics 30: 1312–1313

[2] Walker, J. B., Sytsma, K. J., Treutlein, J. & Wink, M. (2004). Salvia (Lamiaceae) is not monophyletic: Implications for the systematics, radiation, and ecological specializations of Salvia and tribe Mentheae. American *Journal of Botany*, *91*(7), 1115–1125.

[3] Walker, J. B., Drew, B. T. & Sytsma, K. J. (2015). Unravelling Species Relationships and Diversification within the Iconic California Floristic Province Sages Salvia subgenus Audibertia, Lamiaceae). Systematic Botany, *40*(3), 826–844.